

RECEIVED # 13

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TECH CENTER



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/905,744B

DATE: 04/21/2003

TIME: 17:03:14

Input Set : N:\paola\09905744B.txt

Output Set: N:\CRF4\04212003\I905744B.raw

3 <110> APPLICANT: Chadwick, Brian Paul  
 4 Frischauf, Anna Maria  
 6 <111> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES  
 AND NUCLEIC

7 ACIDS

9 &lt;120&gt; FILE REFERENCE: 32110/36120A

11 &lt;140&gt; CURRENT APPLICATION NUMBER: 09/905,744B

12 &lt;141&gt; CURRENT FILING DATE: 2001-07-13

14 &lt;150&gt; PRIOR APPLICATION NUMBER: 09/240,639

15 &lt;151&gt; PRIOR FILING DATE: 1999-01-29

17 &lt;160&gt; NUMBER OF SEQ ID NOS: 32

19 &lt;170&gt; SOFTWARE: PatentIn version 3.1

21 &lt;210&gt; SEQ ID NO: 1

22 &lt;211&gt; LENGTH: 2762

23 &lt;212&gt; TYPE: DNA

24 &lt;213&gt; ORGANISM: Homo Sapiens

26 &lt;216&gt; FEATURE:

27 &lt;221&gt; NAME/KEY: CDS

28 &lt;222&gt; LOCATION: (132)..(1599)

29 &lt;223&gt; OTHER INFORMATION:

W--&gt; 32 &lt;400&gt; 1

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34 aagacccggt gccgcctgct ccccgaaaaa gggaactcgt ctccgtgggt gtggcgaggc      120
35 ggcgggtgca tgaatgggc tatgtgaatg aaaaaaggta tccgttatga aacttcaga      180
36 aaaaagagct acatttttca gcagccgcag cagggtcctt ggcaacaag g atg aga      237
37                                     Met Arg
40                                     1
41
42 aaa ata tca aac cac gga agc ctg cgg gtg gcg aag gtg gca tac ccc      285
43 Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
44                                     10      15
45 cgg ggg ctg tct ctg ggc gtg ttc atc tat gtt gcc tac atc aag tgg      333
46 Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
47                                     25      30
48 car ggg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc      381
49 His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
50                                     40      45      50
51 ccc ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct      429
52 Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
53                                     55      60      65
54 gca gac gga cac gag gtc ttc tac ggt atc atg ttt gat gca gga agc      477
55 Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
56                                     70      75      80
57 acr ggc acc gga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa      525
58 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu

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65	85	90	95	
67	act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt			573
68	Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu			
69	100	105	110	
71	tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa			621
72	Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu			
73	115	120	125	130
75	cta ctg gat gtt gct aaa cag gac att cgg ttc gac ttc tgg aag gcc			669
76	Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala			
77	135	140	145	
79	acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga			717
80	Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly			
81	150	155	160	
83	gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca			765
84	Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala			
85	165	170	175	
87	tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gca aca			813
88	Ser Pro Phe Leu Val Gly Asp Cys Val Ser Ile Met Asn Gly Thr			
89	180	185	190	
91	gat gaa ggc gtt tcg ggg tgg atc acc atc aac ttc ctg aca ggc agc			861
92	Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser			
93	195	200	205	210
95	ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga			909
96	Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly			
97	215	220	225	
99	gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag			957
100	Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln			
101	230	235	240	
103	gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc			1005
104	Ala Ser Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr			
105	245	250	255	
107	tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca			1053
108	Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala			
109	260	265	270	
111	cgc ctg ggc atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga			1101
112	Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly			
113	275	280	285	290
115	aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg			1149
116	Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp			
117	295	300	305	
119	gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca ggc gca			1197
120	Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala			
121	310	315	320	
123	agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt cca aac			1245
124	Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn			
125	325	330	335	
127	aga gtg cac agc acg gag gaa gtg aag cat gtg gac ttc tat gct ttc			1293
128	Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe			
129	340	345	350	

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131 tcc tac tat tac gac att gca gct ggt gtg ggc ctc ata gat ggg gag      1341
132 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
133 355      360      365      370
134 aag gaa gga agc ctg gtg ggg gac ttc gag atc gca gcc aag tac      1389
135 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
136 375      380      385
137 gtt tgt cgg acc ctg gag aca cag ccg cag agt agc ccc ttc tca tgc      1437
138 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
139 390      395      400
140 atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc      1465
141 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
142 405      410      415
143 agg agc aaa atg ctg aag ctc act cgg aaa att gac aat gtt gag acc      1503
144 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
145 420      425      430
146 agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga      1581
147 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
148 435      440      445      450
149 cag aag agt cca gcc tca tagtggaaga gccatccctg tccccgtcag      1629
150 Gln Lys Ser Pro Ala Ser
151 455
152 cagtgtctgt gtgtctgcat aaacccctct gtccctggacg tgacttcate ctgaggagcc      1689
153 acagcacagg ccgtgtggc actttctgca caactgctct gggacttgca gaaggccctgg      1749
154 tctgtccctg gcatcagct ctccacagtea catctggcca gagggtctgc tggacctggg      1809
155 cccctgtctaa tgccactgt ctgcccgggc tccaaagtggg caggaccagg acagaaccac      1869
156 aggcacacac ttagggggca gtgtgctctc ctgcccgtcc catcccatg ccccgctccg      1929
157 ggggtgtgtg ctgctctgt gtatgtccct ggcaggggag tctgtctctc cagcctgtea      1989
158 gtttctctcc cagggcagag ctccccttcc tgcaagagtc tgggaggcgg tgcaggctgt      2049
159 cctggctgt ctggggaagc cgagggaacg ccataacacc cccgggacag taggtctggg      2109
160 cggcaccaact ggaactctg gacttgagtg tctttgtctc tccctgggta tgaatgtgtg      2169
161 agttcaccac gaggcctgt ctctcaccac attgtgtggt ttgggggtta tgatggaggg      2229
162 aqacacctct tcatagacgg caggtgcccc cctttcaggg agtctccag catgggggga      2289
163 tcccgggcat gactgtctgt aaactatttg tggtgtgtct gcttgagtga cgtctctgtc      2349
164 gtgtgggtac caagtgttg ttagaaaact gtgttctgag ccccttttc tggacaccaaa      2409
165 ctgtctctct tgaatgtat gctactgtga gtgttcccg cctagccagg gccatgtctt      2469
166 aggtgcagct gtgccacgg tcagctgagc cacagtccca gaaccaagct ctgggtgtct      2529
167 cgggacacca tccgacacc tcgggtgac cccacccct ccattggacag tgtgagcccc      2589
168 agtgaatgta cagtgcctgg cagagctga acctcatgtg ttccactccc aataaaaagg      2649
169 tgacaggggc tctctcttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa      2709
170 2762
171 <110> SEQ ID NO: 2
172 <111> LENGTH: 456
173 <112> TYPE: PRT
174 <113> ORGANISM: Homo Sapiens
175 <114> SEQUENCE: 2
176 Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala
177 1      5      10      15
178 Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
179 20      25      30

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213 Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
214          35          40          45
217 Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
218          50          55          60
221 Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
222 65          70          75          80
225 Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
226          85          90          95
229 Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
230          100          105          110
233 Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
234          115          120          125
237 Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
238          130          135          140
241 Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
242 145          150          155          160
245 Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
246          165          170          175
249 Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
250          180          185          190
252 Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
253          195          200          205
257 Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
258          210          215          220
261 Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
262 225          230          235          240
265 Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
266          245          250          255
269 Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
270          260          265          270
273 Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
274          275          280          285
277 Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
278          290          295          300
281 Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
282 305          310          315          320
285 Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
286          325          330          335
289 Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
290          340          345          350
293 Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
294          355          360          365
297 Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
298          370          375          380
301 Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
302 385          390          395          400
305 Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
306          405          410          415
309 Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val

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310          420          425          430
311 Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu
314          435          440          445
317 Asn Arg Gln Lys Ser Pro Ala Ser
318          450          455
321 <210> SEQ ID NO: 3
322 <211> LENGTH: 1797
323 <212> TYPE: DNA
324 <213> ORGANISM: Homo Sapiens
326 <220> FEATURE:
327 <221> NAME/KEY: CDS
328 <222> LOCATION: (83)..(1669)
329 <223> OTHER INFORMATION:
W--> 332 <400> 3
333 accacacggt ctggcgcgagg gcgcgctctg cggcagcgct agtcgcttct tccgaatcgg      60
336 ctccgcacacag ctaggagaaaa ag atg ttc act gtg ctg acc cgc caa cca tgt      112
337                               Met Phe Thr Val Leu Thr Arg Gln Pro Cys
337                               1             5             10
339 gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc      160
340 Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
341             15             20             25
343 ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc      208
344 Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
345             30             35             40
347 atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt      256
348 Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
349             45             50             55
351 att gtg ctg gat gcc ggg tot tca aga acc aca gtc tac gtg tat caa      304
352 Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
353             60             65             70
355 tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc      352
356 Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
357 75             80             85             90
359 aaa tgt agt gtg aaa ggc tot gga atc tcc agc tat gga aat aac ccc      400
360 Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
361             95             100             105
363 caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg      448
364 Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
365             110             115             120
367 cag gtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc      496
368 Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
369             125             130             135
371 acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat      544
372 Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
373             140             145             150
375 gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac      592
376 Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
377 155             160             165             170
379 ttt agg ggt gct caa atc att tot ggg caa gaa gaa ggg gta tat gga      640

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**VERIFICATION SUMMARY**PATENT APPLICATION: **US/09/905,744B**

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Input Set : **N:\paola\09905744B.txt**Output Set: **N:\CRF4\04212003\I905744B.raw**

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L:332 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:329  
L:664 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:661  
L:924 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:921